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<110> Sagami Chemical Research Center

5 <120> Human Proteins Having Transmembrane Domains and DNAs Encoding these Proteins

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<150> Japan 9-323129

<151> 1997-11-25

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007620 22045900

35                      40                      45

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255

265

<213> Homo sapiens

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Phe Pro Trp Asn Ile Ile Leu Leu Thr Leu Phe Thr Phe Ala Met Gly

Phe Met Thr Gly Thr Ile Ser Ser Met Tyr Gln Thr Lys Ala Val Ile

Ile Ala Met Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile Phe

10 Cys Phe Gln Thr Lys Val Asp Phe Thr Ser Cys Thr Gly Leu Phe Cys

Val Leu Gly Ile Val Leu Leu Val Thr Gly Ile Val Thr Ser Ile Val

Leu Tyr Phe Gln Tyr Val Tyr Trp Leu His Met Leu Tyr Ala Ala Leu

Gly Ala Ile Cys Phe Thr Leu Phe Leu Ala Tyr Asp Thr Gln Leu Val

Leu Gly Asn Arg Lys His Thr Ile Ser Pro Glu Asp Tyr Ile Thr Gly

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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

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Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp

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Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu

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10           Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser

50           55           60

Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu

65           70           75           80

Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg

15                   85           90           95

Thr Glu Thr Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly

100           105           110

Ala Gln His Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg

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20           Gln Ile Tyr Gly Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe

130           135           140

Leu Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys

145           150           155           160

Thr Gly Thr Leu Val Ala Glu Lys His Val Leu Thr Ala Ala His Cys

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Ile His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val

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001220-224530



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<213> Homo sapiens

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 accatttcca gtatgtacca aaccaaagcc gtcacattg caatgatcat cactgcggtg 600  
 gtatccattt cagtcacat ctctgcttt cagaccaagg tggacttcac ctctgtcaca 660  
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 ctctacttc aatacgttta ctggtccac atgctctatg ctgctctggg ggccatttgt 780  
 ttcacctgt tctggctta cgacacacag ctggtcctgg ggaaccggaa gcacaccatc 840  
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 ttgccccagt ctacctcaa tttagccaag ccagacttg gagccgaagc caaattagaa 180  
 25 gtatcttctt catgtggacc ccagtgtcat aagggaactc cactgcccac ttacgaagag 240  
 gccaaagcaat atctgtctta tgaaacgtc tatgccaatg gcagccgcac agagacgcag 300  
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004230.2.6.9.6.6



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ctg atg ggc acg gcc gag gac ttc gcc gac cag ttc ctc cgt gtc aca 163  
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Glu Ser Ser Pro Lys Gln Tyr Met Gln Leu Gly Gly Arg Val Leu Leu

150            155            160            165  
 gtt ctg atg ttc atg acc ctc ctt cac ttt gac gcc agc ttc ttt tct    643  
 Val Leu Met Phe Met Thr Leu Leu His Phe Asp Ala Ser Phe Phe Ser

                 170            175            180  
 5    att gtc cag aac atc gtg ggc aca gct ctg atg att tta gtg gcc att    691  
 Ile Val Gln Asn Ile Val Gly Thr Ala Leu Met Ile Leu Val Ala Ile  
                  185            190            195

ggt ttt aaa acc aag ctg gct gct ttg act ctt gtt gtg tgg ctc ttt    739  
 Gly Phe Lys Thr Lys Leu Ala Ala Leu Thr Leu Val Val Trp Leu Phe

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 gcc atc aac gta tat ttc aac gcc ttc tgg acc att cca gtc tac aag    787  
 Ala Ile Asn Val Tyr Phe Asn Ala Phe Trp Thr Ile Pro Val Tyr Lys  
                  215            220            225

ccc atg cat gac ttc ctg aaa tac gac ttc ttc cag acc atg tcg gtg    835  
 15    Pro Met His Asp Phe Leu Lys Tyr Asp Phe Phe Gln Thr Met Ser Val  
 230            235            240            245

att ggg ggc ttg ctc ctg gtg gtg gcc ctg ggc cct ggg ggt gtc tcc    883  
 Ile Gly Gly Leu Leu Leu Val Val Ala Leu Gly Pro Gly Gly Val Ser  
                  250            255            260

20    atg gat gag aag aag aag gag tgg taa cagtcacaga tcctacctg    930  
 Met Asp Glu Lys Lys Lys Glu Trp  
                  265

cctggctaag acccgtggcc gtcaaggact gggtcggggt ggattcaaca aaactgccag    990  
 ctttatgta tctcttccc tccccctccc ttggtaaagg cacagatgtt ttgagaactt    1050

25    tatttcaga gacacctgag aatcgatggc tcagtctgct ctggagccac agtctggcgt    1110  
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 agtgaacagc ccgcttggct gtggcatctc agtcctattt ttgagttttt ttgtgggggt    1230

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<212> PRT

<213> Homo sapiens

<400> 8

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Met Gly Gln Asn Asp

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Leu Met Gly Thr Ala Glu Asp Phe Ala Asp Gln Phe Leu Arg Val Thr

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Lys Gln Tyr Leu Pro His Val Ala Arg Leu Cys Leu Ile Ser Thr Phe

15

25 30 35

Leu Glu Asp Gly Ile Arg Met Trp Phe Gln Trp Ser Glu Gln Arg Asp

40 45 50

Tyr Ile Asp Thr Thr Trp Asn Cys Gly Tyr Leu Leu Ala Ser Ser Phe

55 60 65

20

Val Phe Leu Asn Leu Leu Gly Gln Leu Thr Gly Cys Val Leu Val Leu

70 75 80 85

Ser Arg Asn Phe Val Gln Tyr Ala Cys Phe Gly Leu Phe Gly Ile Ile

90 95 100

Ala Leu Gln Thr Ile Ala Tyr Ser Ile Leu Trp Asp Leu Lys Phe Leu

25

105 110 115

Met Arg Asn Leu Ala Leu Gly Gly Gly Leu Leu Leu Leu Ala Glu

120 125 130

007220.2209500

135                      140                      145

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170                      175                      180

185                      190                      195

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250                      255                      260

265

**<211> 2290**

<213> Homo sapiens

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ccctcagccc gtgagcagcc atg tcc aac ccc agc gcc cca cca cca tat gaa 113

1                      5                      10

Asp Arg Asn Pro Leu Tyr Pro Gly Pro Leu Pro Pro Gly Gly Tyr Gly

cag cca tct gtc ctg cca gga ggg tat cct gcc tac cct ggc tac ccg 209

30                      35                      40

10 Gln Pro Gly Tyr Gly His Pro Ala Gly Tyr Pro Gln Pro Met Pro Pro

acc cac ccg atg ccc atg aac tac ggc cca ggc cat ggc tat gat ggg 305

60                      65                      70                      75

Glu Glu Arg Ala Val Ser Asp Ser Phe Gly Pro Gly Glu Trp Asp Asp

cgg aaa gtg cga cac act ttt atc cga aag gtt tac tcc atc atc tcc 401

20                      95                      100                      105

Val Gln Leu Leu Ile Thr Val Ala Ile Ile Ala Ile Phe Thr Phe Val

gaa cct gtc agc gcc ttt gtg agg aga aat gtg gct gtc tac tac gtg 497

125                      130                      135

tcc tat gct gtc ttc gtt gtc acc tac ctg atc ctt gcc tgc tgc cag 545

140                      145                      150                      155

Gly Pro Arg Arg Arg Phe Pro Trp Asn Ile Ile Leu Leu Thr Leu Phe

5                      160                      165                      170

Thr Phe Ala Met Gly Phe Met Thr Gly Thr Ile Ser Ser Met Tyr Gln

175                      180                      185

acc aaa gcc gtc atc att gca atg atc atc act gcg gtg gta tcc att 689

10 Thr Lys Ala Val Ile Ile Ala Met Ile Ile Thr Ala Val Val Ser Ile

190                      195                      200

tca gtc acc atc ttc tgc ttt cag acc aag gtg gac ttc acc tcg tgc 737

Ser Val Thr Ile Phe Cys Phe Gln Thr Lys Val Asp Phe Thr Ser Cys

205                      210                      215

15      aca ggc ctc ttc tgt gtc ctg gga att gtg ctc ctg gtg act ggg att      785

Thr Gly Leu Phe Cys Val Leu Gly Ile Val Leu Leu Val Thr Gly Ile

220                      225                      230                      235

gtc act agc att gtg ctc tac ttc caa tac gtt tac tgg ctc cac atg 833

Val Thr Ser Ile Val Leu Tyr Phe Gln Tyr Val Tyr Trp Leu His Met

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ctc tat gct gct ctg ggg gcc att tgt ttc acc ctg ttc ctg gct tac 881

Leu Tyr Ala Ala Leu Gly Ala Ile Cys Phe Thr Leu Phe Leu Ala Tyr

255                      260                      265

gac aca cag ctg gtc ctg ggg aac cgg aag cac acc atc agc ccc gag 929

25 Asp Thr Gln Leu Val Leu Gly Asn Arg Lys His Thr Ile Ser Pro Glu

270                      275                      280

gac tac atc act ggc gcc ctg cag att tac aca gac atc atc tac atc 977







160                      165                      170

175                      180                      185

190                      195                      200

205                      210                      215

10            220            225            230            235

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270                      275                      280

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<211> 3705

25      <213> Homo sapiens

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Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn  
            35                      40                      45

15      tca tgt gga ccc cag tgt cat aag gga act cca ctg ccc act tac gaa      360  
          Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu  
          65                70                75

cgc aca gag acg cag gtg ggc atc tac atc ctc agc agt agt gga gat 456  
 Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp  
 100 105 110

25 Gly Ala Gln His Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys  
115 120 125  
cgg cag att tat ggc tat gac agc agg ttc agc att ttt ggg aag gac 552

130                      135                      140

Phe Leu Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly

tgc acc ggc acc ctg gtg gca gag aag cat gtc ctc aca gct gcc cac 648

160                      165                      170                      175

10 Cys Ile His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg

gtg ggc ttc cta aag ccc aag ttt aaa gat ggt ggt cga ggg gcc aac 744

195                      200                      205

Asp Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg

gtg aaa cgc acc cat gtg ccc aag ggt tgg atc aag ggc aat gcc aat 840

20                      225                      230                      235

Asp Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro

cac aag aga aaa ttt atg aag att ggg gtg agc cct cct gct aag cag 936

260                      265                      270

ctg cca ggg ggc aga att cac ttc tct ggt tat gac aat gac cga cca 984

275                      280                      285

Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp

ttg ctc tac cag caa tgc gat gcc cag cca ggg gcc agc ggg tct ggg 1080

305                      310                      315

10 Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln Lys Trp Glu Arg Lys

att att ggc att ttt tca ggg cac cag tgg gtg gac atg aat ggt tcc 1176

340                      345                      350

Pro Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala

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<210> 12

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<212> PRT

<213> Homo sapiens

<400> 12

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Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr

20 25 30

Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn

20 35 40 45

Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser

50 55 60

Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu

65 70 75

25 Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser

80 85 90 95

Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp

001250 001250 001250





10